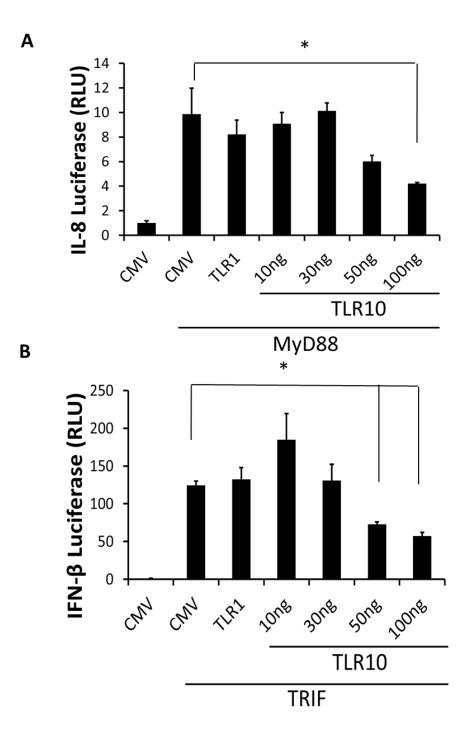
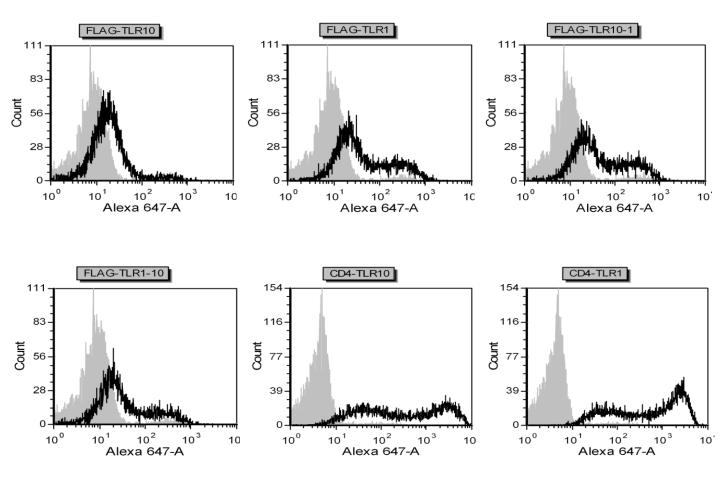
Gene	Fold Change
IL6	-11.65
PELI1	-6.42
TLR3	-5.97
IL1A	-5.88
TLR8	-3.33
LY96	-2.91
IFNB1	-2.70
IL10	-2.34
CD14	-2.31
CXCL10	-2.26
TNF	-2.08
MAP3K1	2.93
TLR9	3.98
HPRT1	-1.52
RPL13A	-1.07
GAPDH	1.03
ACTB	1.23
B2M	1.29

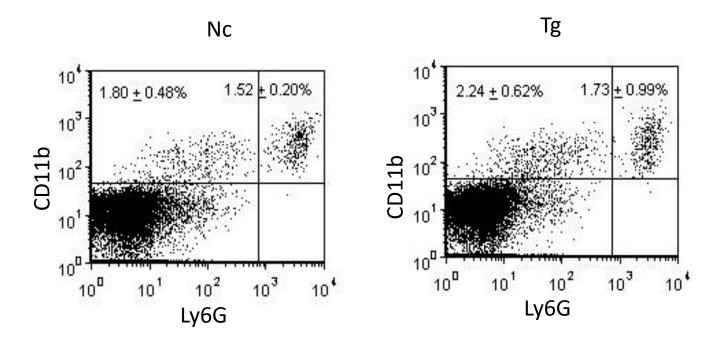
Suppl. Table 1. Down-regulated genes in stably transfected TLR10-U937 cells. TLR10-U937 and MMLV-U937 control cells were differentiated for 48 h in PMA and stimulated with 50 ng/ml PAM₃CSK₄ for 4 h. RNA was isolated and analyzed by real-time PCR for message levels of selected of inflammatory genes. Data represent a subset of the 84 genes tested in the array that, after normalization to house-keeping genes (last 5 rows, italicized), showed greater than 2-fold difference between TLR10 and MMLV control cells. Genes of interest are bolded.



Suppl. Figure 1. Dose-Dependent Suppression of MyD88 and TRIF Signaling by TLR10. HEK293T cells were co-transfected with varying concentrations of TLR10 and either (A) MyD88 and an IL-8 promoter-driven luciferase construct or (B) TRIF and an IFN-β-driven luciferase reporter construct. Results indicate fold induction of luciferase over empty vector after normalizing each sample for transfection efficiency using *Renilla* luciferase. Error bars represent the standard deviation of three independent samples and statistical analysis was performed using two-tailed paired Student's t test. * p< 0.05



Suppl. Figure 2. Cell Surface Expression of TLR Constructs. HEK293T cells were transfected with the indicated FLAG-TLR or CD4-TLR construct and stained with either an anti-FLAG or anti-CD4 antibody. FLAG-TLR and CD4-TLR constructs (black line) show surface expression of each construct compared to MMLV control cells (gray histogram). Cells were gated based upon forward and side scatter characteristics.



Suppl. Figure 3. Whole Blood Monocyte and Neutrophil Populations of TLR10 and Non-Transgenic Mice are Indistinguishable. Monocyte (CD11b⁺ and Ly6G⁻) and neutrophil (CD11b⁺, Ly6G⁺) populations from TLR10 transgenic (tg) and non-transgenic control mice (nc) were assayed by flow cytometry. A representative dot blot from each mouse is shown with averages and standard deviations derived from 6 transgenic mice and 6 non-transgenic mice. Dot plot represents ungated cell populations.